#2   OIPE

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       RAW SEQUENCE LISTING                    DATE: 10/24/2001
       PATENT APPLICATION:  US/09/970,076      TIME: 14:17:42

       Input Set : A:\Uw977451.app
       Output Set: N:\CRF3\10242001\I970076.raw
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   3 <110> APPLICANT: Young, John A.T.
   4        Bradley, Kenneth A.
   5        Collier, Robert J.
   6        Mogridge, Jeremy S.
   8 <120> TITLE OF INVENTION: Anthrax Toxin Receptor
  10 <130> FILE REFERENCE: 960296.97745
C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/970,076
C--> 13 <141> CURRENT FILING DATE: 2001-10-03
  15 <150> PRIOR APPLICATION NUMBER: 60/251,481
  16 <151> PRIOR FILING DATE: 2000-12-05
  18 <160> NUMBER OF SEQ ID NOS: 10
  20 <170> SOFTWARE: PatentIn Ver. 2.1
  22 <210> SEQ ID NO: 1
  23 <211> LENGTH: 1414
  24 <212> TYPE: DNA
  25 <213> ORGANISM: Homo sapiens
  27 <220> FEATURE:
  28 <221> NAME/KEY: CDS
  29 <222> LOCATION: (104)..(1207)
  31 <400> SEQUENCE: 1
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  34 agcgtgggaa ggagcggacc ctgctctccc cgggctgcgg gcc atg gcc acg gcg   115
  35                                                 Met Ala Thr Ala
  36                                                  1
  38 gag cgg aga gcc ctc ggc atc ggc ttc cag tgg ctc tct ttg gcc act   163
  39 Glu Arg Arg Ala Leu Gly Ile Gly Phe Gln Trp Leu Ser Leu Ala Thr
  40   5                  10                  15                  20
  42 ctg gtg ctc atc tgc gcc ggg caa ggg gga cgc agg gag gat ggg ggt   211
  43 Leu Val Leu Ile Cys Ala Gly Gln Gly Gly Arg Arg Glu Asp Gly Gly
  44                  25                  30                  35
  46 cca gcc tgc tac ggc gga ttt gac ctg tac ttc att ttg gac aaa tca   259
  47 Pro Ala Cys Tyr Gly Gly Phe Asp Leu Tyr Phe Ile Leu Asp Lys Ser
  48                  40                  45                  50
  50 gga agt gtg ctg cac cac tgg aat gaa atc tat tac ttt gtg gaa cag   307
  51 Gly Ser Val Leu His His Trp Asn Glu Ile Tyr Tyr Phe Val Glu Gln
  52              55                  60                  65
  54 ttg gct cac aaa ttc atc agc cca cag ttg aga atg tcc ttt att gtt   355
  55 Leu Ala His Lys Phe Ile Ser Pro Gln Leu Arg Met Ser Phe Ile Val
  56      70                  75                  80
  58 ttc tcc acc cga gga aca acc tta atg aaa ctg aca gaa gac aga gaa   403
  59 Phe Ser Thr Arg Gly Thr Thr Leu Met Lys Leu Thr Glu Asp Arg Glu
  60   85                  90                  95                 100
  62 caa atc cgt caa ggc cta gaa gaa ctc cag aaa gtt ctg cca gga gga   451
  63 Gln Ile Arg Gln Gly Leu Glu Glu Leu Gln Lys Val Leu Pro Gly Gly
  64                 105                 110                 115
  66 gac act tac atg cat gaa gga ttt gaa agg gcc agt gag cag att tat   499
  67 Asp Thr Tyr Met His Glu Gly Phe Glu Arg Ala Ser Glu Gln Ile Tyr
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68              120             125             130
70 tat gaa aac aga caa ggg tac agg aca gcc agc gtc atc att gct ttg    547
71 Tyr Glu Asn Arg Gln Gly Tyr Arg Thr Ala Ser Val Ile Ile Ala Leu
72          135             140             145
74 act gat gga gaa ctc cat gaa gat ctc ttt ttc tat tca gag agg gag    595
75 Thr Asp Gly Glu Leu His Glu Asp Leu Phe Phe Tyr Ser Glu Arg Glu
76      150             155             · 160
78 gct aat agg tct cga gat ctt ggt gca att gtt tac tgt gtt ggt gtg    643
79 Ala Asn Arg Ser Arg Asp Leu Gly Ala Ile Val Tyr Cys Val Gly Val
80 165             170             175             180
82 aaa gat ttc aat gag aca cag ctg gcc cgg att gcg gac agt aag gat    691
83 Lys Asp Phe Asn Glu Thr Gln Leu Ala Arg Ile Ala Asp Ser Lys Asp
84          185             190             195
86 cat gtg ttt ccc gtg aat gac ggc ttt cag gct ctg caa ggc atc atc    739
87 His Val Phe Pro Val Asn Asp Gly Phe Gln Ala Leu Gln Gly Ile Ile
88          200             205             210
90 cac tca att ttg aag aag tcc tgc atc gaa att cta gca gct gaa cca    787
91 His Ser Ile Leu Lys Lys Ser Cys Ile Glu Ile Leu Ala Ala Glu Pro
92          215             220             225
94 tcc acc ata tgt gca gga gag tca ttt caa gtt gtc gtg aga gga aac    835
95 Ser Thr Ile Cys Ala Gly Glu Ser Phe Gln Val Val Val Arg Gly Asn
96      230             235             240
98 ggc ttc cga cat gcc cgc aac gtg gac agg gtc ctc tgc agc ttc aag    883
99 Gly Phe Arg His Ala Arg Asn Val Asp Arg Val Leu Cys Ser Phe Lys
100 245            250             255             260.
102 atc aat gac tcg gtc aca ctc aat gag aag ccc ttt tct gtg gaa gac    931
103 Ile Asn Asp Ser Val Thr Leu Asn Glu Lys Pro Phe Ser Val Glu Asp
104            265             270             275
106 act tat tta ctg tgt cca gcg cct atc tta aaa gaa gtt ggc atg aaa    979
107 Thr Tyr Leu Leu Cys Pro Ala Pro Ile Leu Lys Glu Val Gly Met Lys
108            280             285             290
110 gct gca ctc cag gtc agc atg aac gat ggc ctc tct ttt atc tcc agt    1027
111 Ala Ala Leu Gln Val Ser Met Asn Asp Gly Leu Ser Phe Ile Ser Ser
112            295             300             305
114 tct gtc atc atc acc acc aca cac tgt tct gac ggt tcc atc ctg gcc    1075
115 Ser Val Ile Ile Thr Thr Thr His Cys Ser Asp Gly Ser Ile Leu Ala
116      310             315             320
118 atc gcc ctg ctg atc ctg ttc ctg ctc cta gcc ctg gct ctc ctc tgg    1123
119 Ile Ala Leu Leu Ile Leu Phe Leu Leu Leu Ala Leu Ala Leu Leu Trp
120 325            330             335             340
122 tgg ttc tgg ccc ctc tgc tgc act gtg att atc aag gag gtc cct cca    1171
123 Trp Phe Trp Pro Leu Cys Cys Thr Val Ile Ile Lys Glu Val Pro Pro
124            345             350             355
126 ccc cct gcc gag gag agt gag gaa aat aaa ata aaa taacaagaag        1217
127 Pro Pro Ala Glu Glu Ser Glu Glu Asn Lys Ile Lys
128      360             365
130 aagaaagaaa gaaatcccac agaaacagat aacctaacac agcccgtgca acgtatttta 1277
132 tacaatgctc tgaaaatcat agtctcaatc tagacagtct tttcctctag ttccctgtat 1337
134 tcaaatccca gtgtctaaca ttcaataaat agctatatga aatcaaaaaa aaaaaaaaaa 1397
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RAW SEQUENCE LISTING   DATE: 10/24/2001
PATENT APPLICATION: US/09/970,076   TIME: 14:17:42

Input Set : A:\Uw977451.app
Output Set: N:\CRF3\10242001\I970076.raw

136 aaaaaaaaaa aaaaaaa   1414
139 <210> SEQ ID NO: 2
140 <211> LENGTH: 368
141 <212> TYPE: PRT
142 <213> ORGANISM: Homo sapiens
144 <400> SEQUENCE: 2
145 Met Ala Thr Ala Glu Arg Arg Ala Leu Gly Ile Gly Phe Gln Trp Leu
146 1   5   10   15
148 Ser Leu Ala Thr Leu Val Leu Ile Cys Ala Gly Gln Gly Gly Arg Arg
149   20   25   30
151 Glu Asp Gly Gly Pro Ala Cys Tyr Gly Gly Phe Asp Leu Tyr Phe Ile
152   35   40   45
154 Leu Asp Lys Ser Gly Ser Val Leu His His Trp Asn Glu Ile Tyr Tyr
155   50   55   60
157 Phe Val Glu Gln Leu Ala His Lys Phe Ile Ser Pro Gln Leu Arg Met
158 65   70   75   80
160 Ser Phe Ile Val Phe Ser Thr Arg Gly Thr Thr Leu Met Lys Leu Thr
161   85   90   95
163 Glu Asp Arg Glu Gln Ile Arg Gln Gly Leu Glu Glu Leu Gln Lys Val
164   100   105   110
166 Leu Pro Gly Gly Asp Thr Tyr Met His Glu Gly Phe Glu Arg Ala Ser
167   115   120   125
169 Glu Gln Ile Tyr Tyr Glu Asn Arg Gln Gly Tyr Arg Thr Ala Ser Val
170   130   135   140
172 Ile Ile Ala Leu Thr Asp Gly Glu Leu His Glu Asp Leu Phe Phe Tyr
173 145   150   155   160
175 Ser Glu Arg Glu Ala Asn Arg Ser Arg Asp Leu Gly Ala Ile Val Tyr
176   165   170   175
178 Cys Val Gly Val Lys Asp Phe Asn Glu Thr Gln Leu Ala Arg Ile Ala
179   180   185   190
181 Asp Ser Lys Asp His Val Phe Pro Val Asn Asp Gly Phe Gln Ala Leu
182   195   200   205
184 Gln Gly Ile Ile His Ser Ile Leu Lys Lys Ser Cys Ile Glu Ile Leu
185   210   215   220
187 Ala Ala Glu Pro Ser Thr Ile Cys Ala Gly Glu Ser Phe Gln Val Val
188 225   230   235   240
190 Val Arg Gly Asn Gly Phe Arg His Ala Arg Asn Val Asp Arg Val Leu
191   245   250   255
193 Cys Ser Phe Lys Ile Asn Asp Ser Val Thr Leu Asn Glu Lys Pro Phe
194   260   265   270
196 Ser Val Glu Asp Thr Tyr Leu Leu Cys Pro Ala Pro Ile Leu Lys Glu
197   275   280   285
199 Val Gly Met Lys Ala Ala Leu Gln Val Ser Met Asn Asp Gly Leu Ser
200   290   295   300
202 Phe Ile Ser Ser Ser Val Ile Ile Thr Thr Thr His Cys Ser Asp Gly
203 305   310   315   320
205 Ser Ile Leu Ala Ile Ala Leu Leu Ile Leu Phe Leu Leu Leu Ala Leu
206   325   330   335
208 Ala Leu Leu Trp Trp Phe Trp Pro Leu Cys Cys Thr Val Ile Ile Lys

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209              340            345            350
211 Glu Val Pro Pro Pro Pro Ala Glu Glu Ser Glu Glu Asn Lys Ile Lys
212          355            360            365
216 <210> SEQ ID NO: 3
217 <211> LENGTH: 180
218 <212> TYPE: PRT
219 <213> ORGANISM: Artificial Sequence
221 <220> FEATURE:
222 <223> OTHER INFORMATION: Description of Artificial Sequence:von Willebrand
223       factor A domain consensus sequence
225 <400> SEQUENCE: 3
226 Pro Leu Asp Val Val Phe Leu Leu Asp Gly Ser Gly Ser Met Gly Gly
227 1             5            10            15
229 Asn Arg Phe Glu Leu Ala Lys Glu Phe Val Leu Lys Leu Val Glu Gln
230          20            25            30
232 Leu Asp Ile Gly Pro Arg Gly Asp Arg Val Gly Leu Val Thr Phe Ser
233          35            40            45
235 Ser Asp Ala Arg Val Leu Phe Pro Leu Asn Asp Ser Gln Ser Lys Asp
236       50            55            60
238 Ala Leu Leu Glu Ala Leu Ala Asn Leu Ser Tyr Ser Leu Gly Gly Gly
239 65            70         .   75            80
241 Thr Asn Leu Gly Ala Ala Leu Glu Tyr Ala Leu Glu Asn Leu Phe Ser
242          85            90            95
244 Glu Ser Ala Gly Ser Arg Arg Gly Ala Pro Lys Val Leu Ile Leu Ile
245          100           105           110
247 Thr Asp Gly Glu Ser Asn Asp Gly Gly Glu Asp Ile Leu Lys Ala Ala
248          115           120           125
250 Lys Glu Leu Lys Arg Ser Gly Val Lys Val Phe Val Val Gly Val Gly
251    130           135           140
253 Asn Ala Val Asp Glu Glu Glu Leu Lys Lys Leu Ala Ser Ala Pro Gly
254 145           150           155           160
256 Gly Val Phe Ala Val Glu Asp Leu Pro Glu Leu Leu Asp Leu Leu Ile
257          165           170           175
259 Asp Leu Leu Leu
260          180
263 <210> SEQ ID NO: 4
264 <211> LENGTH: 198
265 <212> TYPE: PRT
266 <213> ORGANISM: Homo sapiens
268 <400> SEQUENCE: 4
269 Cys Pro Ser Leu Ile Asp Val Val Val Cys Asp Glu Ser Asn Ser
270 1             5            10            15
272 Ile Tyr Pro Trp Asp Ala Val Lys Asn Phe Leu Glu Lys Phe Val Gln
273          20            25            30
275 Gly Leu Asp Ile Gly Pro Thr Lys Thr Gln Val Gly Leu Ile Gln Tyr
276          35            40            45
278 Ala Asn Asn Pro Arg Val Val Phe Asn Leu Asn Thr Tyr Lys Thr Lys
279       50            55            60
281 Glu Glu Met Ile Val Ala Thr Ser Gln Thr Ser Gln Tyr Gly Gly Asp
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Input Set : A:\Uw977451.app
Output Set: N:\CRF3\10242001\I970076.raw

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282  65                       70                  75                      80
284  Leu Thr Asn Thr Phe Gly Ala Ile Gln Tyr Ala Arg Lys Tyr Ala Tyr
285                   85                  90                      95
287  Ser Ala Ser Gly Gly Arg Arg Ser Ala Ala Thr Lys Val Met Val Val
288                  100                 105                 110
290  Val Thr Asp Gly Glu Ser His Asp Gly Ser Met Leu Lys Ala Val Ile
291          115                 120                 125
293  Asp Gln Cys Asn His Asp Asn Ile Leu Arg Phe Gly Ile Ala Val Leu
294      130                 135                 140
296  Gly Tyr Leu Asn Arg Asn Ala Leu Asp Thr Lys Asn Leu Ile Lys Glu
297  145                 150                 155                 160
299  Ile Lys Ala Ile Ala Ser Ile Pro Thr Glu Arg Tyr Phe Phe Asn Val
300                  165                 170                 175
302  Ser Asp Glu Ala Ala Leu Leu Glu Lys Ala Gly Thr Leu Gly Glu Gln
303                  180                 185                 190
305  Ile Phe Ser Ile Glu Gly
306              195
309  <210> SEQ ID NO: 5
310  <211> LENGTH: 5540
311  <212> TYPE: DNA
312  <213> ORGANISM: Homo sapiens
314  <220> FEATURE:
315  <221> NAME/KEY: CDS
316  <222> LOCATION: (144)..(1835)
318  <400> SEQUENCE: 5
319  aattgcttcc ggggagttgc gagggagcga gggggaataa aggacccgcg aggaagggcc 60
321  cgcggatggc gcgtccctga gggtcgtggc gagttcgcgg agcgtgggaa ggagcggacc 120
323  ctgctctccc cgggctgcgg gcc atg gcc acg gcg gag cgg aga gcc ctc ggc 173
324                          Met Ala Thr Ala Glu Arg Arg Ala Leu Gly
325                           1               5                   10
327  atc ggc ttc cag tgg ctc tct ttg gcc act ctg gtg ctc atc tgc gcc 221
328  Ile Gly Phe Gln Trp Leu Ser Leu Ala Thr Leu Val Leu Ile Cys Ala
329                   15                  20                  25
331  ggg caa ggg gga cgc agg gag gat ggg ggt cca gcc tgc tac ggc gga 269
332  Gly Gln Gly Gly Arg Arg Glu Asp Gly Gly Pro Ala Cys Tyr Gly Gly
333                   30                  35                  40
335  ttt gac ctg tac ttc att ttg gac aaa tca gga agt gtg ctg cac cac 317
336  Phe Asp Leu Tyr Phe Ile Leu Asp Lys Ser Gly Ser Val Leu His His
337              45                  50                  55
339  tgg aat gaa atc tat tac ttt gtg gaa cag ttg gct cac aaa ttc atc 365
340  Trp Asn Glu Ile Tyr Tyr Phe Val Glu Gln Leu Ala His Lys Phe Ile
341      60                  65                  70
343  agc cca cag ttg aga atg tcc ttt att gtt ttc tcc acc cga gga aca 413
344  Ser Pro Gln Leu Arg Met Ser Phe Ile Val Phe Ser Thr Arg Gly Thr
345  75                  80                  85                  90
347  acc tta atg aaa ctg aca gaa gac aga gaa caa atc cgt caa ggc cta 461
348  Thr Leu Met Lys Leu Thr Glu Asp Arg Glu Gln Ile Arg Gln Gly Leu
349                   95                 100                 105
351  gaa gaa ctc cag aaa gtt ctg cca gga gga gac act tac atg cat gaa 509
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VERIFICATION SUMMARY   DATE: 10/24/2001
PATENT APPLICATION: US/09/970,076   TIME: 14:17:43

Input Set : A:\Uw977451.app
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L:12 M:270 C: Current Application Number differs, Replaced Application Number
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date